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SEARCH REQUEST FORM

7-27

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Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevent citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevent claim(s).

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Type of Search

_____ N.A. Sequence

_____ A.A. Sequence

_____ Structure

_____ Bibliographic

Vendors

_____ IG

_____ STN

_____ Dialog

_____ APS

_____ Geninfo

_____ SDC

_____ DARC/Questel

_____ Other

PTO-1590 (8-90)

STIC-Biotech/ChemLib

7-27

From: Teng, Sally
To: STIC-Biotech/ChemLib
Subject: 08/426,509
Date: Thursday, July 10, 1997 10:17AM

Interference Search

Please search SEQ ID NO: 1-6

31	75	16.2	256	17	R85919	Human GRB-3.	1.04e+01
32	75	16.2	536	8	R39706	Human pp60 c-src prot	1.04e+01
33	74	15.9	501	18	W03760	Mullerian inhibiting	1.28e+01
34	74	15.9	505	8	R41921	MISR2A/MISR2B.	1.28e+01
35	74	15.9	505	10	R55369	Human Activin recepto	1.28e+01
36	74	15.9	505	13	R70240	Serine/threonine kina	1.28e+01
37	74	15.9	505	10	R55373	Mouse Activin recepto	1.28e+01
38	71	15.3	1290	15	R90583	Phospholipase C-gamma	2.41e+01
39	70	15.1	128	13	R64261	MAb L243 light chain	2.96e+01
40	70	15.1	128	12	R64231	MAb L243 VL region.	2.96e+01
41	69	14.9	509	16	R94601	TAR-1 polypeptide.	3.64e+01
42	68	14.7	86	11	R56775	Human anti-haemophili	4.46e+01
43	68	14.7	2332	2	P71728	Facor VIII:c variant	4.46e+01
44	68	14.7	2351	3	P60741	Sequence of human fac	4.46e+01
45	68	14.7	2351	13	R78223	Human Factor-VIII:c.	4.46e+01

ALIGNMENTS

RESULT 1
ID R71129 standard; Protein; 64 AA.
AC R71129;
DT 27-OCT-1995 (first entry)
DE SH3 domain of cytoplsmic tyrosine kinase.
KW cytoplasmic; tyrosine kinase; blood; cell differentiation;
KW screening; anticancer agent; SH3; src homology domain.
OS Homo sapiens.
PN WO9506113-A.
PD 02-MAR-1995.
PF 25-AUG-1994; J01411.
PR 25-AUG-1993; JP-210403.
PR 29-MAR-1994; JP-058553.
PA (ASAH) ASAHI KASEI KOGYO KK.
PI Sakano S;
DR WPI; 95-106842/14.
DR N-PSDB; Q84888.
PT Cytoplasmic tyrosine kinase and antibody recognising it - for
PT screening chemical substances for tyrosine kinase inhibitory or
PT activating activity for use as cancer therapy
PS Claim 1; Page 38; 58pp; English.
CC A cytoplasmic tyrosine kinase which has enhanced expression in
CC connection with blood cell differentiation has been isolated from the
CC human UT-7 blood cell line. This sequence comprises the SH3 (src
CC homology) domain of the enzyme (residues 7-70 of R71132; residues
CC 48-111 of R71133). The DNA sequences and antibodies raised against
CC the enzyme, are usful for screening agents for inhibiting or activating
CC activity on the tyrosine kinase, for use as anticancer agents.
SQ Sequence 64 AA;

Query Match 100.0%; Score 464; DB 13; Length 64;
Best Local Similarity 100.0%; Pred. No. 1.20e-44;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 apgtqcitkcehtrpkpgelafrkgdvvtileacenkswyrvkhhtsgqegllaagalre 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     48 APGTQCITKCEHTRPKPGELAFRKGDVVTILEACENKSWYRVKHHTSGQEGLLAAGALRE 107

Db     61 real 64
          ||||
Qy    108 REAL 111
```

RESULT 2
ID R71132 standard; Protein; 466 AA.
AC R71132;
DT 27-OCT-1995 (first entry)

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Feb 3 16:52:10 1997; MasPar time 2.72 Seconds
                                    241.839 Million cell updates/sec
Tabular output not generated.

Title: >US-08-426-509-2
Description: (48-111) from US08426509.pep (1 of 4)
Perfect Score: 464
Sequence: 1 APGTQCITKCEHTRPKPGEL.....HTSGQEGLLAAGALREREAL 64

Scoring table: PAM 150
                Gap 11

Searched: 88003 seqs, 10295656 residues

Post-processing: Minimum Match 0%
                  Listing first 45 summaries

Database: a-geneseq25
             1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
             8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
             14:part14 15:part15 16:part16 17:part17 18:part18

Statistics: Mean 25.991; Variance 87.600; scale 0.297

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	464	100.0	64	13	R71129	SH3 domain of cytopls	1.20e-44
2	464	100.0	466	13	R71132	N-terminal truncated	1.20e-44
3	464	100.0	507	13	R71133	Cytoplsmic tyrosine k	1.20e-44
4	460	99.1	507	15	R84181	Megakaryocyte kinase	3.71e-44
5	113	24.4	217	17	R85918	Human GRB-2.	1.83e-03
6	112	24.1	176	13	R71943	Grb3-3 protein.	2.32e-03
7	104	22.4	217	15	R84636	Grb2 protein.	1.55e-02
8	100	21.6	620	17	R94535	ITK tyrosine kinase.	3.93e-02
9	98	21.1	821	7	R35451	Mouse eps8.	6.25e-02
10	95	20.5	659	17	R94534	BTK tyrosine kinase.	1.25e-01
11	90	19.4	317	5	R26061	Growth Factor Recepto	3.88e-01
12	87	18.8	212	10	R53543	Thyroid hormone recep	7.60e-01
13	85	18.3	303	17	R77439	Mouse CRKL protein.	1.19e+00
14	84	18.1	466	13	R71910	Erythroid p55.	1.48e+00
15	81	17.5	475	6	R31046	Rat D1B dopamine rece	2.86e+00
16	80	17.2	963	18	R84082	Thermostable enzyme (	3.55e+00
17	78	16.8	78	9	R46684	Fragment 273-351 of G	5.47e+00
18	78	16.8	516	9	R46685	Peptide P9 inhibits r	5.47e+00
19	78	16.8	533	8	R39705	Chicken pp60 c-src pr	5.47e+00
20	78	16.8	844	5	R25671	Mouse vav proto oncog	5.47e+00
21	78	16.8	870	11	R59924	Human GAP protein.	5.47e+00
22	78	16.8	1047	5	R25336	Lambda clone 101 prot	5.47e+00
23	78	16.8	1047	2	R06328	Sequence of full leng	5.47e+00
24	78	16.8	1047	2	R11137	GAP6 encoded by lambd	5.47e+00
25	77	16.6	298	15	R84183	Megakaryocyte kinase	6.78e+00
26	77	16.6	390	15	R83825	p47(phox) protein.	6.78e+00
27	77	16.6	505	15	R85929	Protein tyrosine-kina	6.78e+00
28	77	16.6	505	8	R41941	pTK gene LpTK-2 prod.	6.78e+00
29	76	16.4	61	11	R60993	Fragment of p56lck co	8.40e+00
30	76	16.4	1713	13	R70148	Deduced sequence of c	8.40e+00

DE N-terminal truncated cytoplsmic tyrosine kinase.
KW cytoplasmic; tyrosine kinase; blood; cell differentiation;
KW screening; anticancer agent; SH3; src homology domain.
OS Homo sapiens.
FH Key   Location/Qualifiers
FT Domain   7..70
FT /note= "SH3 domain"
FT Domain   81..155
FT /note= "SH2 domain"
FT Domain   192..438
FT /note= "tyrosine kinase domain"
PN WO9506113-A.
PD 02-MAR-1995.
PF 25-AUG-1994; J01411.
PR 25-AUG-1993; JP-210403.
PR 29-MAR-1994; JP-058553.
PA (ASAH) ASAHI KASEI KOGYO KK.
PI Sakano S;
DR WPI; 95-106842/14.
DR N-PSDB; Q84888.
PT Cytoplasmic tyrosine kinase and antibody recognising it - for
PT screening chemical substances for tyrosine kinase inhibitory or
PT activating activity for use as cancer therapy
PS Claim 1; Page 40-42; 58pp; English.
CC A cytoplasmic tyrosine kinase which has enhanced expression in
CC connection with blood cell differentiation has been isolated from the
CC human UT-7 blood cell line. This sequence comprises an N-terminal
CC truncated fragment of the enzyme (residues 42-507 of R71133). The DNA
CC sequences and antibodies raised against the enzyme, are usful for
CC screening agents for inhibiting or activating activity on the tyrosine
CC kinase, for use as anticancer agents.
SQ Sequence 466 AA;

  Query Match   100.0%; Score 464; DB 13; Length 466;
  Best Local Similarity 100.0%; Pred. No. 1.20e-44;
  Matches   64; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Db   7 apgtqcitkcehtrpkpgelafrkgdvvtileacenkswyrvkhhtsgqegllaagalre 66
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   48 APGTQCITKCEHTRPKPGELAFRKGDVVTILEACENKSWYRVKHHTSGQEGLLAAGALRE 107

Db   67 real 70
          ||||
Qy   108 REAL 111

RESULT 3
ID R71133 standard; Protein; 507 AA.
AC R71133;
DT 27-OCT-1995 (first entry)
DE Cytoplsmic tyrosine kinase.
KW cytoplasmic; tyrosine kinase; blood; cell differentiation;
KW screening; anticancer agent; SH3; src homology domain.
OS Homo sapiens.
FH Key   Location/Qualifiers
FT Domain   48..111
FT /note= "SH3 domain"
FT Domain   122..196
FT /note= "SH2 domain"
FT Domain   233..478
FT /note= "tyrosine kinase domain"
PN WO9506113-A.
PD 02-MAR-1995.
PF 25-AUG-1994; J01411.
PR 25-AUG-1993; JP-210403.
PR 29-MAR-1994; JP-058553.

PA (ASAH) ASAHI KASEI KOGYO KK.
PI Sakano S;
DR WPI; 95-106842/14.
DR N-PSDB; Q84888.
PT Cytoplasmic tyrosine kinase and antibody recognising it - for
PT screening chemical substances for tyrosine kinase inhibitory or
PT activating activity for use as cancer therapy
PS Claim 1; Page 42-44; 58pp; English.
CC A cytoplasmic tyrosine kinase which has enhanced expression in
CC connection with blood cell differentiation has been isolated from the
CC human UT-7 blood cell line. The DNA sequences and antibodies raised
CC against the enzyme, are usful for screening agents for inhibiting or
CC activating activity on the tyrosine kinase, for use as anticancer agents.
SQ Sequence 507 AA;

Query Match 100.0%; Score 464; DB 13; Length 507;
Best Local Similarity 100.0%; Pred. No. 1.20e-44;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db     48 apgtqcitkcehtrpkpgelafrkgdvvtileacenkswyrvkhhtsgqegllaagalre 107
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     48 APGTQCITKCEHTRPKPGELAFRKGDVVTILEACENKSWYRVKHHTSGQEGLLAAGALRE 107

Db    108 real 111
          ||||
Qy    108 REAL 111
```

RESULT 4
ID R84181 standard; Protein; 507 AA.
AC R84181;
DT 26-MAR-1996 (first entry)
DE Megakaryocyte kinase MKK1.
KW Megakaryocyte kinase-1; MKK1; cytoplasmic tyrosine kinase;
KW cellular signal transduction; leukaemia; thrombocytopenia.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Domain 48..111
FT /label= SH3_domain
FT Domain 122..196
FT /label= SH2_domain
FT Domain 233..478
FT /label= Catalytic_domain
PN WO9529185-A1.
PD 02-NOV-1995.
PF 24-APR-1995; U05008.
PR 22-APR-1994; US-232545.
PR 21-APR-1995; US-426509.
PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
PA (SUGE-) SUGEN INC.
PI Gishizky M, Sures I, Ullrich A;
DR WPI; 95-382959/49.
DR N-PSDB; T00616.
PT New poly:nucleotide(s) encoding megakaryocyte tyrosine kinase(s) -
PT used to develop prods. for the treatment and diagnosis of kinase
PT related signal transduction abnormalities.
PS Claim 15; Fig 1A-C; 82pp; English.
CC Human megakaryocyte kinase MKK1 (R84181) is a 58 kDa cytosolic
CC tyrosine kinase showing 54% homology with csk. It appears to play
CC a regulatory role in the growth and differentiation of
CC megakaryocytes and perhaps neural tissues. Recombinant MKK1 can be
CC produced in host cells by expression of encoding cDNA (T00616), and
CC used in the treatment and diagnosis of e.g. leukaemia and
CC thrombocytopenia.
SQ Sequence 507 AA;

```
  Query Match           99.1%;  Score 460;  DB 15;  Length 507;
  Best Local Similarity  98.4%;  Pred. No. 3.71e-44;
  Matches    63;  Conservative    1;  Mismatches   0;  Indels   0;  Gaps   0;

Db      48 apgtqcitkcehtrpkpgelafrkgdvvtileacenkswyrvkhhtsgeegllaagalre 107
           ||||||||||||||||||||||||||||||||||||||||||||||||:||||||||||||
Qy      48 APGTQCITKCEHTRPKPGELAFRKGDVVTILEACENKSWYRVKHHTSG@EGLLAAGALRE 107

Db     108 real 111
           ||||
Qy     108 REAL 111


RESULT    5
ID   R85918 standard; Protein; 217 AA.
AC   R85918;
DT   16-MAY-1996  (first entry)
DE   Human GRB-2.
KW   GRB-2; growth factor receptor bound; tyrosine kinase; regulation;
KW   cell growth; cellular metabolism; screening; signal transduction;
KW   cancer; diabetes; CORT technique; cloning of receptor targets.
OS   Homo sapiens.
PN   WO9524426-A1.
PD   14-SEP-1995.
PF   13-MAR-1995; U03385.
PR   11-MAR-1994; US-208887.
PA   (UYNY ) UNIV NEW YORK STATE.
PI   Margolis BL,  Schlessinger J,  Skolnik EY;
DR   WPI; 95-328235/42.
DR   N-PSDB; T07167.
PT   DNA encoding tyrosine kinase-binding proteins - used to screen
PT   agents capable of modulating cell growth or cellular metabolism
PS   Disclosure; Fig 26A-C; 215pp; English.
CC   Using a new cloning technique, CORT (cloning of receptor targets)
CC   several new tyrosine kinase (TK) binding proteins were isolated. Growth
CC   factor receptor bound proteins GRB-1,GRB-2, GRB-3, GRB-4, GRB-7 and
CC   GRB-10 were isolated using this method. This sequence represents GRB-2.
CC   The proteins bind to a tyrosine-phosphorylated domain of a eukaryotic
CC   TK. GRB proteins can be used for screening agents which are capable
CC   of modulating cell growth that occurs via signal transduction through
CC   TKs. Such agents can be used to prevent or inhibit cell growth or to
CC   counteract tumour development. GRB proteins are also useful for
CC   identifying susceptibility to diseases asociated with alterations in
CC   cellular metabolism mediated by TK pathways e.g. cancer and diabetes.
SQ   Sequence   217 AA;

  Query Match           24.4%;  Score 113;  DB 17;  Length 217;
  Best Local Similarity  33.3%;  Pred. No. 1.83e-03;
  Matches    12;  Conservative   11;  Mismatches  11;  Indels   2;  Gaps   2;

Db       4 iakydfkataddelsfkrgdilkvlneecdqn-wyk 38
           |:| :       ||:|::||:: :| | |: : ||:
Qy      54 ITKCEHTRPKPGELAFRKGDVVTIL-EACENKSWYR 88


RESULT    6
ID   R71943 standard; Protein; 176 AA.
AC   R71943;
DT   17-OCT-1995  (first entry)
DE   Grb3-3 protein.
KW   Grb3-3; cancer; apoptosis; AIDS; gene therapy.
OS   Homo sapiens.
PN   WO9507981-A.
PD   23-MAR-1995.
PF   09-MAY-1994; F00542.
PR   15-SEP-1993; FR-010971.
```

PA (RHON) RHONE POULENC RORER SA.
PI Schweighoffer F, Tocque B;
DR WPI; 95-131349/17.
DR N-PSDB; Q89211.
PT New human Grb3-3 gene and vectors contg. it - useful in control
PT of cell death etc. partic. for treating cancer and AIDS
PS Disclosure; Page 15-16; 31pp; French.
CC A probe derived from the Grb2 gene was used to screen a library of
CC human placental DNA in lambda-gt10. A positive clone contained the
CC sequence for the novel gene, Grb3-3, an isoform of Grb2 (deleted
CC SH2 domain). In vivo delivery of the Grb3-3 gene (or variants,
CC including antisense sequences) using viral vectors can interfere
CC with proliferation, differentiation and/or death of cells.
SQ Sequence 176 AA;

Query Match 24.1%; Score 112; DB 13; Length 176;
Best Local Similarity 30.6%; Pred. No. 2.32e-03;
Matches 11; Conservative 12; Mismatches 11; Indels 2; Gaps 2;

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Db      4 iakydfkataddd lsfkrgdilkvlneecdqn-wyk 38
          |:| :       :|:|::||:: :| | |: : ||:
Qy     54 ITKCEHTRPKPGELAFRKGDVVTIL-EACENKSWYR 88
```

RESULT 7
ID R84636 standard; Protein; 217 AA.
AC R84636;
DT 25-FEB-1996 (first entry)
DE Grb2 protein.
KW Grb2; BCR-ABL; tyrosine kinase; transformation; Ras; oncoprotein;
KW leukaemia.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Domain 5..55
FT /label= SH3_domain
FT Domain 60..157
FT /label= SH2_domain
FT Domain 163..214
FT /label= SH3_domain
PN CA2113494-A.
PD 15-JUL-1995.
PF 14-JAN-1994; 113494.
PR 14-JAN-1994; CA-113494.
PA (MOUN) MOUNT SINAI HOSPITAL CORP.
PA (TEXA) UNIV TEXAS.
PI Arlinghaus R, Gish G, Liu J, Pawson A, Puil L;
DR WPI; 95-302931/40.
DR N-PSDB; T05108.
PT Detection of agents that modify BCR-ABL mediated transformation -
PT useful in treatment of leukaemia and other malignancies
PS Example 1; Page 48; 106pp; English.
CC The human Grb2 protein (R84636) acts as an adaptor to link BCR-ABL
CC tyrosine-kinase to mSos1 (R84638). The resulting BCR-ABL-Grb2-mSos1
CC complex activates the Ras pathway leading to morphological
CC transformation. Substances that affect this transformation are
CC useful in the treatment of chronic, acute myelogenous or acute
CC lymphocytic leukaemia, and are identified by reaction with
CC Grb2 (or its SH2 or SH3 domains) and with a cpd. contg. the Brb2-
CC binding site on BCR-ABL, Sos or Shc and examination of any resulting
CC complex.
SQ Sequence 217 AA;

Query Match 22.4%; Score 104; DB 15; Length 217;
Best Local Similarity 27.8%; Pred. No. 1.55e-02;
Matches 10; Conservative 13; Mismatches 11; Indels 2; Gaps 2;

```
Db      4 iakydfkataddelsfkradilkvlnqecdqn-wyk 38
          |:| :       ||:|:::|:: :| : |: : ||:
Qy     54 ITKCEHTRPKPGELAFRKGDVVTIL-EACENKSWYR 88


RESULT    8
ID   R94535 standard; Protein; 620 AA.
AC   R94535;
DT   10-JUL-1996  (first entry)
DE   ITK tyrosine kinase.
KW   Cytoplasmic tyrosine kinase; BMX; haematopoietic cell;
KW   cell growth; cell proliferation; tumour; diagnosis; therapy; ITK.
OS   Mus musculus.
PN   WO9611275-A1.
PD   18-APR-1996.
PF   09-OCT-1995; FI0555.
PR   07-OCT-1994; US-320432.
PA   (UYHE-) UNIV HELSINKI LICENSING LTD OY.
PI   Alitalo K;
DR   WPI; 96-209856/21.
PT   Cytoplasmic tyrosine kinase BMX and related DNA - useful to
PT   stimulate haematopoietic cell growth.
PS   Disclosure; Page 23-25; 40pp; English.
CC   Cytoplasmic tyrosine kinase ITK (R94535) is selectively expressed
CC   at certain stages of T-cell development.  The sequences of ITK
CC   and 2 other members of a newly-identified non-receptor tyrosine
CC   kinase family, BTK (R94534) and TEC (R94536), and of the
CC   Drosophila Src28C tyrosine kinase (R94538), were compared with
CC   that of novel cytoplasmic tyrosine kinase BMX (see also R94533).
CC   Close homology was found.
SQ   Sequence   620 AA;

  Query Match           21.6%;  Score 100;  DB 17;  Length 620;
  Best Local Similarity 29.1%;  Pred. No. 3.93e-02;
  Matches   16;  Conservative   16;  Mismatches  21;  Indels   2;  Gaps   2;

Db    177 ialydyqtndpqelalrrneeycllдsseih-wwrvqdr-nghegyvpssylvek 229
          |:  :     | |||:|: :   :|:: |   | ||  : :|:|| ::::: | |:
Qy     54 ITKCEHTRPKPGELAFRKGDVVTILEACENKSWYRVKHHTSGQEGLLAAGALRER 108


RESULT    9
ID   R35451 standard; Protein; 821 AA.
AC   R35451;
DT   25-AUG-1993  (first entry)
DE   Mouse eps8.
KW   Epidermal growth factor receptor; EGFR-pathway substrate; eps;
KW   tyrosine kinase receptor; TKR; SH2; SH3; mitogenesis.
OS   Mus musculus.
PN   US7935311-A.
PD   01-APR-1993.
PF   25-AUG-1992; 935311.
PR   25-AUG-1992; US-935311.
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICE.
PI   Di Fiore PP,  Fazioli F;
DR   WPI; 93-159477/19.
DR   N-PSDB; Q40730.
PT   Epidermal growth factor receptor substrate, eps 8 - used to
PT   enhance mitogenic response of cells to epidermal growth factor
PS   Disclosure; Page 30-37; 40pp; English.
CC   Eps8 is a novel EGFR substrate.  The protein bears the
CC   characteristic signatures of TKR substrates including SH2 and
CC   SH3 domains.  Eps8 is involved in the transduction of mitogenic
CC   signals and it can be used to enhance the mitogenic response of
CC   cells to EGF.
SQ   Sequence   821 AA;
```

```
  Query Match           21.1%;  Score 98;  DB 7;  Length 821;
  Best Local Similarity  27.5%;  Pred. No. 6.25e-02;
  Matches    14;  Conservative   18;  Mismatches  16;  Indels   3;  Gaps   2;

Db    537 skydfvarnsselsvnkddvleild--drrqwwkvrn-asgdsgfvpnnil 584
          :| :    :::||:  | ||: ||:  : : | :|:: :||: |:::   |
Qy     55 TKCEHTRPKPGELAFRKGDVVTILEACENKSWYRVKHHTSGQEGLLAAGAL 105


RESULT   10
ID   R94534 standard; Protein; 659 AA.
AC   R94534;
DT   10-JUL-1996  (first entry)
DE   BTK tyrosine kinase.
KW   Cytoplasmic tyrosine kinase; BMX; haematopoietic cell;
KW   cell growth; cell proliferation; tumour; diagnosis; therapy; BTK.
OS   Mus musculus.
FH   Key             Location/Qualifiers
FT   Domain          1..219
FT   /label= N-terminal_region
FT   /note= "the N-terminal region contains the
FT   pleckstrin homology region consisting
FT   of a 7-strand antiparallel beta-sheet"
FT   Domain          220..272
FT   /label= SH3_domain
FT   Domain          281..336
FT   /label= SH2_domain
FT   Domain          407..644
FT   /label= Tyrosine-kinase_domain
FT   Binding_site    408..430
FT   /label= ATP-binding_region
FT   Modified_site   551
FT   /label= Autophosphorylation_site
PN   WO9611275-A1.
PD   18-APR-1996.
PF   09-OCT-1995; FI0555.
PR   07-OCT-1994; US-320432.
PA   (UYHE-) UNIV HELSINKI LICENSING LTD OY.
PI   Alitalo K;
DR   WPI; 96-209856/21.
PT   Cytoplasmic tyrosine kinase BMX and related DNA - useful to
PT   stimulate haematopoietic cell growth.
PS   Disclosure; Page 21-23; 40pp; English.
CC   Cytoplasmic tyrosine kinase BTK (R94534) is selectively expressed
CC   at certain stages of B-cell development.  The sequences of BTK
CC   and 2 other members of a newly-identified non-receptor tyrosine
CC   kinase family, ITK (R94535) and TEC (R94536), and of the
CC   Drosophila Src28C tyrosine kinase (R94538), were compared with
CC   that of novel cytoplasmic tyrosine kinase BMX (see also R94533).
CC   Close homology was found.
SQ   Sequence   659 AA;

  Query Match           20.5%;  Score 95;  DB 17;  Length 659;
  Best Local Similarity  36.2%;  Pred. No. 1.25e-01;
  Matches    17;  Conservative   11;  Mismatches  17;  Indels   2;  Gaps   2;

Db    229 nandlqlrkgdeyfilees-nlpwwrard-kngqegyipsnyvteae 273
          :: :| :||||   |||   | :| | :   :|||| :::  : | |
Qy     63 KPGELAFRKGDVVTILEACENKSWYRVKHHTSGQEGLLAAGALRERE 109


RESULT   11
ID   R26061 standard; Protein; 317 AA.
AC   R26061;
DT   02-FEB-1993  (first entry)
```

DE Growth Factor Receptor Bound protein GRB-2 partial sequence.
KW Tyrosine phophorylation; epidermal growth factor receptor; EGFR;
KW src homology domain; SH2; SH3.
OS Homo sapiens.
FH Key   Location/Qualifiers
FT Domain   30
FT /note= "start of SH2 domain"
FT Domain   133
FT /note= "start of SH3 domain"
FT Misc_difference 183
FT /note= "corresponds to CNG codon,
FT where N is unknown"
FT Misc_difference 184
FT /note= "corresponds to TGA codon"
FT Misc_difference 196
FT /note= "corresponds to TAA codon"
FT Misc_difference 199
FT /note= "corresponds to TGA codon"
FT Misc_difference 215
FT /note= "corresponds to TGA codon"
FT Misc_difference 231
FT /note= "corresponds to TGA codon"
FT Misc_difference 202
FT /note= "corresponds to TAA codon"
FT Misc_difference 299
FT /note= "corresponds to TGA codon"
FT Misc_difference 301
FT /note= "corresponds to TAA codon"
FT Misc_difference 302
FT /note= "corresponds to TAA codon"
FT Misc_difference 315
FT /note= "corresponds to TAG codon"
PN WO9213001-A.
PD 06-AUG-1992.
PF 17-JAN-1992; U00434.
PR 18-JAN-1991; US-643237.
PA (UYNY) UNIV NEW YORK STATE.
PI Margolis BL, Schlessinger J, Skolnik EY;
DR WPI; 92-284605/34.
DR N-PSDB; Q27255.
PT Probe from tyrosine-phosphorylated portion of receptor tyrosine
PT kinase - used for detection of proteins capable of binding to
PT receptors, useful for e.g. identifying susceptibility to cancer
PT and diabetes
PS Claim 18; Fig 16; 86pp; English.
CC The GRB-2 partial coding sequence was isolated from human brain stem
CC lambda gt11 expression library by screening with tyrosine
CC phosphorylated C-terminal tail of the EGF Receptor. The amino acid
CC sequence deduced from the nucleotide sequence (the "ORF" includes
CC several nonsense codons !) contains unique SH2 and SH3 domains.
CC See also Q27254.
SQ Sequence 317 AA;

  Query Match   19.4%; Score 90; DB 5; Length 317;
  Best Local Similarity 36.4%; Pred. No. 3.88e-01;
  Matches   8; Conservative   8; Mismatches   6; Indels   0; Gaps   0;

Db   143 gelgfrrgdfihvadnsdpnww 164
          |||:||:|| : ::: : : |
Qy   65 GELAFRKGDVVTILEACENKSW 86

RESULT 12
ID R53543 standard; protein; 212 AA.
AC R53543;
DT 21-FEB-1995 (first entry)

DE Thyroid hormone receptor-interacting protein - S410a
KW nuclear thyroid hormone interacting proteins; TR; JL1; JL2; S410a;
KW transcriptional coactivator; treatment; diagnosis; SH3 domains;
KW thyroid related disorders; modulation; thyroid hormone receptor;
KW nuclear hormone receptor; isolation.
OS Chimeric Homo sapiens.
OS Chimeric Bacterial sp.
FH Key   Location/Qualifiers
FT Misc_difference 116
FT /note= "stop codon encoded by TGA"
PN WO9410338-A.
PD 11-MAY-1994.
PF 29-OCT-1993; U10443.
PR 30-OCT-1992; US-969136.
PA (GEHO) GEN HOSPITAL CORP.
PI Lee JW, Moore DD;
DR WPI; 94-199808/24.
PT Nuclear hormone receptor interacting polypeptides, esp. thyroid
PT hormone=interacting proteins (TRs) - for identifying proteins
PT useful in treatment and diagnosis of thyroid related disorders by
PT inoculating thyroid hormone receptor activity
PS Claim 21; Page 50-51; 105pp; English.
CC This sequence shows the partial amino acid sequence of S410a
CC (containing a SH3 domain), a thyroid hormone (TR) interacting protein.
CC TR-interacting proteins physically associate with thyroid hormone
CC receptor. Nearly all the fusion cDNAs showed very strong dependence
CC on hormone activation. The proteins can be used in an in vivo trap
CC system for the isolation of proteins which associate with any nuclear
CC hormone receptor. The proteins and Abs may be used to treat or diagnose
CC thyroid disorders, and to modulate thyroid hormone receptor activity.
SQ Sequence 212 AA;

  Query Match   18.8%; Score 87; DB 10; Length 212;
  Best Local Similarity 22.0%; Pred. No. 7.60e-01;
  Matches   13; Conservative   20; Mismatches 25; Indels   1; Gaps   1;

Db   54 spighcvaiyhfegssegtismaegedlslneedkgdgwtrvrrkegg-egyvptsylr 111
          :| :|::   : | :: |: ::::| :| ||:: :| || :::: ||
Qy   48 APGTQCITKCEHTRPKPGELAFRKGDVVTILEACENKSWYRVKHHTSGQEGLLAAGALR 106

RESULT 13
ID R77439 standard; Protein; 303 AA.
AC R77439;
DT 21-JUL-1996 (first entry)
DE Mouse CRKL protein.
KW Mouse CRKL protein; tyrosine phosphorylation; diagnosis;
KW chronic myelogenous leukaemia; acute lymphoblastic leukaemia;
KW Philadelphia chromosome; BCL; ABL; treatment.
OS Mus musculus.
FH Key   Location/Qualifiers
FT Binding_site
FT Domain   9..103
FT /note= "SH2 domain""
FT Domain   131..179
FT /note= "N-terminal SH3 domain"
FT Modified_site   193..210
FT /note= "tyrosine phosphorylation site"
FT Domain   238..290
FT /note= "C-terminal SH3 domain"
PN WO9531545-A2.
PD 23-NOV-1995.
PF 12-MAY-1995; U05957.
PR 13-MAY-1994; US-242513.
PA (CHIL-) CHILDRENS HOSPITAL LOS ANGELES.
PI Groffen JH, Heisterkamp NC, Ten Hoeve J;

DR WPI; 96-010931/01.
DR N-PSDB; T04144.
PT Diagnosis of tyrosine phosphorylated CRKL protein cancers - by
PT detecting increased level of CRKL protein or CRKL binding protein,
PT also compsns. for treating chronic myelogenous leukaemia.
PS Claim 37; Fig 10b; 74pp; English.
CC The mouse CRKL protein may be used in the diagnosis of Philadelphia
CC chromosome-positive leukaemias. For example, since CRKL is clearly
CC tyrosine-phosphorylated in chronic myelogenous leukaemia and
CC Philadelphia chromosome (Ph)-positive acute lymphoblastic leukaemia
CC patients expressing the BCR/ABL protein, but not in BCR-ABL-negative
CC peripheral blood cells, tyrosine-phosphorylation of CRKL may be used
CC as a diagnostic indicator for BCL/ABL activity in Ph-positive
CC leukaemia. Thus, overexpression of tyrosine-phosphorylated CRKL
CC protein, or an increase in protein, gene copy number or mRNA is
CC indicative of Ph-positive leukaemia. Fragments of the CRKL protein
CC may also be used in the treatment of individuals with cancers
CC arising from cells which express the CRKL protein by inhibition of
CC the synthesis or activity of the CRKL protein.
SQ Sequence 303 AA;

  Query Match   18.3%; Score 85; DB 17; Length 303;
  Best Local Similarity 27.8%; Pred. No. 1.19e+00;
  Matches   10; Conservative   14; Mismatches 10; Indels   2; Gaps   2;

Db   141 dlpfkkgellviiekpeeq-wwsarn-kdgrvgnip 174
          :|:|:||::: |:| |: | :: |: |:::
Qy   66 ELAFRKGDVVTILEACENKSWYRVKHHTSGQEGLLA 101

RESULT 14
ID R71910 standard; Protein; 466 AA.
AC R71910;
DT 25-SEP-1995 (first entry)
DE Erythroid p55.
KW Erythroid p55; erythrocyte membrane protein; hemolytic anemia;
KW Dyskeratosis congenita; cancer; diagnosis; therapy.
OS Homo sapiens.
FH Key   Location/Qualifiers
FT Region   163..233
FT /label= SH3_motif
FT Domain   267..420
FT /label= Guanylate-kinase
PN US5401835-A.
PD 28-MAR-1995.
PF 31-JUL-1992; 923739.
PR 31-JUL-1992; US-923739.
PA (CHIS/) CHISHTI A H.
PI Chishti AH;
DR WPI; 95-138985/18.
DR N-PSDB; Q87925.
PT New human erythroid p55 nucleic acids - used to develop products
PT for diagnosis and treatment of p55 abnormalities, and for cancer
PT treatment
PS Claim 1; Column 23-28; 31pp; English.
CC A human reticulocyte lambda-gt11 cDNA library was screened using
CC rabbit polyclonal antibodies against purified native p55. Positive
CC plaques were purified and phage DNA was analyzed and used to prepare
CC probes. Human erthrocyte plasma membrane extracts were analyzed to
CC obtain DNA (given in Q87925) encoding p55 (R71910).
SQ Sequence 466 AA;

  Query Match   18.1%; Score 84; DB 13; Length 466;
  Best Local Similarity 27.7%; Pred. No. 1.48e+00;
  Matches   13; Conservative   14; Mismatches 19; Indels   1; Gaps   1;

```
Db    180 keaglkfatgdiiqiinkddsnwwqgrvegsskesaglipspelqew 226
          | : | |  ||:: |::  :::: |  ||   :    ||:::  |:|:
Qy     63 KPGELAFRKGDVVTILEACENKSWY-RVKHHTSG@EGLLAAGALRER 108


RESULT   15
ID   R31046 standard; Protein; 475 AA.
AC   R31046;
DT   26-MAY-1993  (first entry)
DE   Rat D1B dopamine receptor.
KW   PCR; amplify; degenerate; primer; TM; transmembrane region; human; D1;
KW   dopamine; receptor; probe; rat; pBLUESCRIPT II SK+; testis; DR5; D1B;
KW   genomic library; lambdaDASH II; Kozak; consensus sequence; V-15.
OS   Rattus rattus.
PN   WO9218533-A.
PD   29-OCT-1992.
PF   16-APR-1992; U03187.
PR   16-APR-1991; US-686591.
PA   (UYDU-) UNIV DUKE.
PI   Caron MG,  Jarvie KR,  Tiberi M;
DR   WPI; 93-036060/04.
DR   N-PSDB; Q35148.
PT   Cloned gene encoding rat D1b dopamine receptor - used to screen
PT   cpds. for receptor activity or in receptor binding assays
PS   Disclosure; Page 25-28; 39pp; English.
CC   This sequence represents rat D1B dopamine receptor.  The DNA
CC   sequence encoding this polypeptide was isolated using the primer
CC   sequences given in Q35146-47.  These oligomers are degenerate primers
CC   corresponding to the 5th and 6th transmembrane (TM) regions of the
CC   human D1 dopamine receptor.  These primers were used to amplify
CC   sheared human DNA and the amplification products were subcloned into
CC   the sequencing vector pBLUESCRIPT II SK+.  A 230bp fragment (V-15) was
CC   found to correspond to the 5th TM region, the 3rd intracellular loop
CC   and the 6th TM region.  V-15 was used as a template for the synthesis
CC   of a 32P-labeled probe. This probe was used to screen a rat testis
CC   genomic library in lambdaDASH II.  One isolated clone (DR5) had an
CC   open reading frame of 1425 bp (475 amino acids) which contained the
CC   full coding sequence for rat D1B-dopamine receptor.  The predicted
CC   encoded protein has a molecular weight of 52834.  The putative
CC   initiator methionine was selected on the basis of the best Kozak
CC   consensus sequence found in frame with the remainer of the coding
CC   block and preceded by a stop codon.
SQ   Sequence   475 AA;

  Query Match           17.5%;  Score 81;  DB 6;  Length 475;
  Best Local Similarity  47.8%;  Pred. No. 2.86e+00;
  Matches    11;  Conservative    5;  Mismatches   7;  Indels   0;  Gaps   0;

Db    177 nwhrdkagsqgqegllsngtpwe 199
          :| | |  : ||||||: |: :|
Qy     85 SWYRVKHHTSG@EGLLAAGALRE 107


Search completed: Mon Feb  3 16:52:22 1997
Job time : 12 secs.
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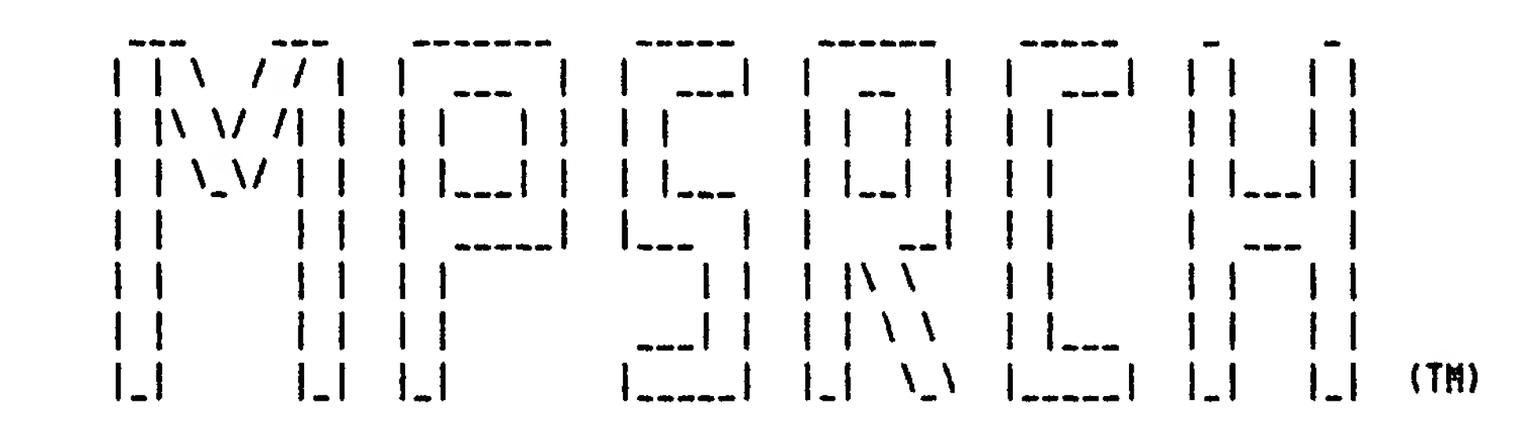

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Feb 3 16:51:25 1997; MasPar time 4.09 Seconds
402.449 Million cell updates/sec
Tabular output not generated.

Title: >US-08-426-509-2
Description: (48-111) from US08426509.pep (1 of 4)
Perfect Score: 464
Sequence: 1 APGTQCITKCEHTRPKPGEL.....HTSGQEGLLAAGALREREAL 64

Scoring table: PAM 150
Gap 11

Searched: 82182 seqs, 25727515 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: pir48
1:ann1 2:ann2 3:ann3 4:unann1 5:unann2 6:unann3 7:unann4
8:unann5 9:unann6 10:unann7 11:unann8 12:unann9 13:unenc
14:unrev

Statistics: Mean 35.059; Variance 66.115; scale 0.530

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	464	100.0	507	4	A55625	protein-tyrosine kin	7.24e-76
2	449	96.8	527	11	A49865	protein-tyrosine kin	1.16e-72
3	420	90.5	465	4	B55625	protein-tyrosine kin	1.72e-66
4	403	86.9	465	12	I48926	protein-tyrosine kin	6.85e-63
5	165	35.6	450	4	A41973	protein-tyrosine kin	7.64e-15
6	161	34.7	450	12	I48929	protein-tyrosine kin	4.17e-14
7	161	34.7	450	1	S15094	protein-tyrosine kin	4.17e-14
8	161	34.7	450	1	JH0559	protein-tyrosine kin	4.17e-14
9	125	26.9	468	10	S46791	hypothetical protein	1.02e-07
10	116	25.0	211	10	A46444	SH2-SH3 adaptor prot	3.33e-06
11	115	24.8	217	11	JT0664	growth factor recept	4.88e-06
12	113	24.4	217	12	A54688	modular adaptor Grb2	1.04e-05
13	113	24.4	217	12	S26050	gene ash protein - r	1.04e-05
14	113	24.4	217	11	A43321	growth factor recept	1.04e-05
15	112	24.1	2415	10	A33733	spectrin alpha chain	1.52e-05
16	111	23.9	451	10	S58653	hypothetical protein	2.21e-05
17	110	23.7	452	10	S46798	hypothetical protein	3.22e-05
18	110	23.7	505	4	S24550	protein-tyrosine kin	3.22e-05
19	110	23.7	506	4	S24553	protein-tyrosine kin	3.22e-05
20	102	22.0	228	10	S25730	sem-5 protein - Caen	6.12e-04
21	102	22.0	527	12	A55631	protein-tyrosine kin	6.12e-04
22	100	21.6	512	4	A39719	protein-tyrosine kin	1.26e-03
23	100	21.6	620	4	S33253	protein-tyrosine kin	1.26e-03
24	99	21.3	442	11	A45184	B cell progenitor ki	1.80e-03
25	98	21.1	507	4	A39939	protein-tyrosine kin	2.57e-03

26	98	21.1	821	12	S39983	eps8 protein - mouse	2.57e-03
27	97	20.9	968	12	S46992	protein p130 - rat	3.67e-03
28	97	20.9	2429	2	SJHUA	spectrin alpha chain	3.67e-03
29	96	20.7	467	14	A57627	p55 erythrocyte memb	5.22e-03
30	95	20.5	509	4	A23639	protein-tyrosine kin	7.42e-03
31	95	20.5	509	1	OKHULK	protein-tyrosine kin	7.42e-03
32	95	20.5	659	11	I37212	Bruton agammaglobuli	7.42e-03
33	95	20.5	659	12	B45184	B cell progenitor ki	7.42e-03
34	95	20.5	659	11	S28912	protein-tyrosine kin	7.42e-03
35	95	20.5	660	12	JN0471	protein-tyrosine kin	7.42e-03
36	92	19.8	512	1	TVHULY	protein-tyrosine kin	2.11e-02
37	89	19.2	303	5	S41754	CRKL protein - human	5.87e-02
38	88	19.0	1244	9	S25327	cytoskeleton assembl	8.23e-02
39	87	18.8	377	11	S08636	nck protein - human	1.15e-01
40	87	18.8	532	4	B34104	protein-tyrosine kin	1.15e-01
41	87	18.8	534	4	A44991	protein-tyrosine kin	1.15e-01
42	87	18.8	534	4	S33568	protein-tyrosine kin	1.15e-01
43	87	18.8	537	1	TVHUSR	protein-tyrosine kin	1.15e-01
44	87	18.8	537	1	TVHUSY	protein-tyrosine kin	1.15e-01
45	87	18.8	1099	11	S31926	myosin IB heavy chai	1.15e-01

ALIGNMENTS

```
RESULT    1
ENTRY             A55625     #type complete
TITLE             protein-tyrosine kinase (EC 2.7.1.112),
                    megakoryocyte-associated - human
ORGANISM          #formal_name Homo sapiens #common_name man
DATE              24-Feb-1995 #sequence_revision 24-Feb-1995 #text_change
                    01-Mar-1996
ACCESSIONS        A55625; S43533
REFERENCE         A55625
   #authors       Avraham, S.; Jiang, S.; Ota, S.; Fu, Y.; Deng, B.; Dowler,
                    L.L.; White, R.A.; Avraham, H.
   #journal       J. Biol. Chem. (1995) 270:1833-1842
   #title         Structural and functional studies of the intracellular
                    tyrosine kinase MATK gene and its translated product.
   #accession     A55625
      ##status         preliminary; not compared with conceptual translation
      ##molecule_type DNA
      ##residues       1-507 ##label AVR
REFERENCE         S43533
   #authors       Sakano, S.; Iwama, A.; Inazawa, J.; Ariyama, T.; Ohno, M.;
                    Suda, T.
   #journal       Oncogene (1994) 9:1155-1161
   #title         Molecular cloning of a novel non-receptor tyrosine kinase,
                    HYL (hematopoietic consensus tyrosine-lacking kinase).
   #accession     S43533
      ##status         preliminary
      ##molecule_type mRNA
      ##residues       1-507 ##label SAK
      ##cross-references EMBL:X77278
GENETICS
   #gene          GDB:MATK
      ##cross-references GDB:G00-304-667
CLASSIFICATION    #superfamily SH2 homology; protein kinase homology; SH3
                    homology
KEYWORDS          phosphotransferase
FEATURE
   55-105              #domain SH3 homology #label SH31\
   122-211             #domain SH2 homology #label SH2\
   233-485             #domain protein kinase homology #label KIN
SUMMARY           #length 507  #molecular-weight 56469  #checksum 6051

  Query Match           100.0%;  Score 464;  DB 4;  Length 507;
```

```
  Best Local Similarity 100.0%;  Pred. No. 7.24e-76;
  Matches    64;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db     48 apgtqcitkcehtrpkpgelafrkgdvvtileacenkswyrvkhhtsgqegllaagalre 107
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     48 APGTQCITKCEHTRPKPGELAFRKGDVVTILEACENKSWYRVKHHTSGQEGLLAAGALRE 107

Db    108 real 111
          ||||
Qy    108 REAL 111


RESULT    2
ENTRY             A49865     #type complete
TITLE             protein-tyrosine kinase (EC 2.7.1.112) matk - human
ALTERNATE_NAMES   megakaryocyte-associated tryosine kinase
ORGANISM          #formal_name Homo sapiens #common_name man
DATE              30-Jun-1995 #sequence_revision 30-Jun-1995 #text_change
                    19-Oct-1995
ACCESSIONS        A49865
REFERENCE         A49865
   #authors       Bennett, B.D.; Cowley, S.; Jiang, S.; London, R.; Deng, B.;
                    Grabarek, J.; Groopman, J.E.; Goeddel, D.V.; Avraham, H.
   #journal       J. Biol. Chem. (1994) 269:1068-1074
   #title         Identification and characterization of a novel tyrosine
                    kinase from megakaryocytes.
   #accession     A49865
      ##status         preliminary
      ##molecule_type mRNA
      ##residues       1-527 ##label BEN
      ##cross-references GB:L18974
CLASSIFICATION    #superfamily SH2 homology; protein kinase homology; SH3
                    homology
KEYWORDS          phosphotransferase
FEATURE
   55-105             #domain SH3 homology #label SH31\
   122-211            #domain SH2 homology #label SH2\
   233-484            #domain protein kinase homology #label KIN
SUMMARY           #length 527  #molecular-weight 58473  #checksum 1630

  Query Match           96.8%;  Score 449;  DB 11;  Length 527;
  Best Local Similarity  96.9%;  Pred. No. 1.16e-72;
  Matches    62;  Conservative    1;  Mismatches   1;  Indels   0;  Gaps   0;

Db     48 apgtqcitkcehtrpkpgelafrkgdvvtileacenkswyrvkhhtsgqegllaagalrd 107
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:
Qy     48 APGTQCITKCEHTRPKPGELAFRKGDVVTILEACENKSWYRVKHHTSGQEGLLAAGALRE 107

Db    108 geal 111
           |||
Qy    108 REAL 111


RESULT    3
ENTRY             B55625     #type complete
TITLE             protein-tyrosine kinase (EC 2.7.1.112),
                    megakoryocyte-associated - mouse
ORGANISM          #formal_name Mus musculus #common_name house mouse
DATE              24-Feb-1995 #sequence_revision 24-Feb-1995 #text_change
                    19-Oct-1995
ACCESSIONS        B55625
REFERENCE         A55625
   #authors       Avraham, S.; Jiang, S.; Ota, S.; Fu, Y.; Deng, B.; Dowler,
                    L.L.; White, R.A.; Avraham, H.
   #journal       J. Biol. Chem. (1995) 270:1833-1842
   #title         Structural and functional studies of the intracellular
```

```
                  tyrosine kinase MATK gene and its translated product.
   #accession    B55625
      ##status        preliminary; not compared with conceptual translation
      ##molecule_type mRNA
      ##residues      1-465 ##label AVR
CLASSIFICATION   #superfamily SH3 homology; protein kinase homology; SH2
                  homology
KEYWORDS         phosphotransferase
FEATURE
   13-63              #domain SH3 homology #label SH31\
   80-169             #domain SH2 homology #label SH2\
   191-443            #domain protein kinase homology #label KIN
SUMMARY          #length 465  #molecular-weight 51585  #checksum 6919

  Query Match           90.5%;  Score 420;  DB 4;  Length 465;
  Best Local Similarity  85.9%;  Pred. No. 1.72e-66;
  Matches    55;  Conservative    7;  Mismatches   2;  Indels   0;  Gaps   0;

Db       6 apgtqcmtkcensrpkpgelafrkgdmvtileacedkswyrakhhgsgqegllaaaalrq 65
           ||||||:||||::|||||||||||||:||||||||:||||| ||| ||||||||||:|||:
Qy      48 APGTQCITKCEHTRPKPGELAFRKGDVVTILEACENKSWYRVKHHTSGQEGLLAAGALRE 107

Db      66 real 69
           ||||
Qy     108 REAL 111


RESULT    4
ENTRY            I48926     #type complete
TITLE            protein-tyrosine kinase (EC 2.7.1.112) Ctk - mouse
ALTERNATE_NAMES  csk-type protein-tyrosine kinase
ORGANISM         #formal_name Mus musculus #common_name house mouse
DATE             15-Mar-1996 #sequence_revision 15-Mar-1996 #text_change
                  15-Mar-1996
ACCESSIONS       I48926
REFERENCE        A53469
   #authors      Klages, S.; Adam, D.; Class, K.; Fargnoli, J.; Bolen, J.B.;
                  Penhallow, R.C.
   #journal      Proc. Natl. Acad. Sci. U.S.A. (1994) 91:2597-2601
   #title        Ctk: a protein-tyrosine kinase related to Csk that defines an
                  enzyme family.
   #cross-references MUID:94195789
   #accession    I48926
      ##status        preliminary
      ##molecule_type mRNA
      ##residues      1-465 ##label RES
      ##cross-references EMBL:U05210; NID:g450232; CDS_PID:g450233
KEYWORDS         phosphotransferase
SUMMARY          #length 465  #molecular-weight 51495  #checksum 6748

  Query Match           86.9%;  Score 403;  DB 12;  Length 465;
  Best Local Similarity  84.4%;  Pred. No. 6.85e-63;
  Matches    54;  Conservative    6;  Mismatches   4;  Indels   0;  Gaps   0;

Db       6 apgtqcmtkcensrpkpgelafrkgdmvtileacedkswyrakhhgsgqegllaaaalrh 65
           ||||||:||||::|||||||||||||:||||||||:||||| ||| ||||||||||:|||
Qy      48 APGTQCITKCEHTRPKPGELAFRKGDVVTILEACENKSWYRVKHHTSGQEGLLAAGALRE 107

Db      66 geal 69
              |||
Qy     108 REAL 111


RESULT    5
ENTRY            A41973     #type fragment
TITLE            protein-tyrosine kinase (EC 2.7.1.112) CSK - chicken
```

```
  Query Match           39.5%;  Score 711;  DB 15;  Length 675;
  Best Local Similarity  42.2%;  Pred. No. 6.42e-56;
  Matches  105;  Conservative   54;  Mismatches  82;  Indels   8;  Gaps   7;

Db    415 eeitllkelgsgqfgvvqlgkwkgqydvavkmikegsmsedeffqeaqtmmklshpklvk 474
          : :||  ::| |:|| |  |   ||  |||| ||   :: : |::|:  | |: | :||:
Qy    233 QHLTLGAQIGEGEFGAVLQGEYLGQ-KVAVKNIK-CDVTAQAFLDETAVMTKMQHENLVR 290

Db    475 fygvcskeypiyivteyisngcllnylrshgkgl-epsqllemcydvcegmafleshqfi 533
          : ||   :  :||| | :|:| |:|:||::|::| : :|||:    | ||| :|||  ::
Qy    291 LLGVILHQ-GLYIVMEHVSKGNLVNFLRTRGRALVNTAQLLQFSLHVAEGMEYLESKKLV 349

Db    534 hrdlaarnclvdrdlcvkvsdfgmtryvlddqyvssvgtkfpvkwsapevfhyfkyssks 593
          |||||||| ||  ||  ||||||:::   :   : |  :::||||:||| :   |::|||
Qy    350 HRDLAARNILVSEDLVAKVSDFGLAK-A-ERKGLDS--SRLPVKWTAPEALKHGKFTSKS 405

Db    594 dvwafgilmwevfslgkqpydlydnsqvvlkvsqghrlyrphlasdtiyqimyscwhelp 653
          |||:||:|:||||| |: ||      :|   |  | |:  |   :  :  :| |||   |
Qy    406 DVWSFGVLLWEVFSYGRAPYPKMSLKEVSEAVEKGYRMEPPEGCPGPVHVLMSSCWEAEP 465

Db    654 ekrptfqql 662
          :|| |: |
Qy    466 ARRPPFRKL 474


Search completed: Mon Feb  3 16:58:35 1997
Job time : 26 secs.
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      ___    ___    ______    _____    _____    _____    _      _
     | | \  / / |  |  ___ |  |  ___|  |  __ |  |  ___|  | |    | |
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     | |      | |  | |          ___| |  | | \ \  | |___   | |   | |
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               Distribution rights by IntelliGenetics, Inc.

MPsrch_pp   protein - protein database search, using Smith-Waterman algorithm

Run on:           Mon Feb  3 16:57:28 1997;  MasPar time 9.41 Seconds
                                             672.791 Million cell updates/sec
Tabular output not generated.

Title:            >US-08-426-509-2
Description:      (233-478) from US08426509.pep (2 of 4)
Perfect Score:    1798
Sequence:         1 QHLTLGAQIGEGEFGAVLQG.........SCWEAEPARRPPFRKLAEKL 246

Scoring table:    PAM 150
                  Gap 11

Searched:         82182 seqs, 25727515 residues

Post-processing:  Minimum Match 0%
                  Listing first 45 summaries

Database:         pir48
                    1:ann1 2:ann2 3:ann3 4:unann1 5:unann2 6:unann3 7:unann4
```

8:unann5 9:unann6 10:unann7 11:unann8 12:unann9 13:unenc
14:unrev

Statistics: Mean 45.505; Variance 121.033; scale 0.376

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	1798	100.0	507	4	A55625	protein-tyrosine kin	3.01e-257
2	1730	96.2	465	4	B55625	protein-tyrosine kin	2.05e-246
3	1730	96.2	465	12	I48926	protein-tyrosine kin	2.05e-246
4	1683	93.6	527	11	A49865	protein-tyrosine kin	6.22e-239
5	1160	64.5	450	4	A41973	protein-tyrosine kin	3.91e-156
6	1148	63.8	450	1	JH0559	protein-tyrosine kin	3.01e-154
7	1145	63.7	450	1	S15094	protein-tyrosine kin	8.92e-154
8	1125	62.6	450	12	I48929	protein-tyrosine kin	1.24e-150
9	838	46.6	507	4	A39939	protein-tyrosine kin	7.94e-106
10	837	46.6	1520	1	TVFFA	protein-tyrosine kin	1.14e-105
11	821	45.7	542	11	A49114	protein-tyrosine kin	3.41e-103
12	817	45.4	509	1	OKHULK	protein-tyrosine kin	1.42e-102
13	816	45.4	1146	4	B35962	protein-tyrosine kin	2.03e-102
14	816	45.4	1182	4	A35962	protein-tyrosine kin	2.03e-102
15	814	45.3	557	10	A00629	protein-tyrosine kin	4.13e-102
16	812	45.2	697	7	A26132	gag-abl-pol polyprot	8.43e-102
17	812	45.2	1130	1	TVHUA	protein-tyrosine kin	8.43e-102
18	811	45.1	505	1	TVHUHC	protein-tyrosine kin	1.20e-101
19	809	45.0	526	4	S20808	protein-tyrosine kin	2.45e-101
20	808	44.9	981	1	FOMVGM	gag-abl polyprotein	3.50e-101
21	808	44.9	1123	4	A39962	kinase-related trans	3.50e-101
22	803	44.7	509	4	A23639	protein-tyrosine kin	2.08e-100
23	804	44.7	526	7	S26420	src protein - Rous s	1.45e-100
24	804	44.7	526	7	S20676	protein-tyrosine kin	1.45e-100
25	803	44.7	526	1	OKFVYR	protein-tyrosine kin	2.08e-100
26	803	44.7	536	4	S33569	protein-tyrosine kin	2.08e-100
27	802	44.6	526	1	TVFVR	protein-tyrosine kin	2.97e-100
28	800	44.5	537	4	A43806	protein-tyrosine kin	6.04e-100
29	799	44.4	537	1	TVHUSY	protein-tyrosine kin	8.63e-100
30	799	44.4	541	1	TVCHYS	protein-tyrosine kin	8.63e-100
31	799	44.4	568	1	TVFVS1	protein-tyrosine kin	8.63e-100
32	796	44.3	528	1	TVFVG9	protein-tyrosine kin	2.51e-99
33	794	44.2	526	4	S15582	protein-tyrosine kin	5.11e-99
34	794	44.2	533	1	TVCHS	protein-tyrosine kin	5.11e-99
35	793	44.1	537	1	TVHUSR	protein-tyrosine kin	7.29e-99
36	793	44.1	539	11	B49114	protein-tyrosine kin	7.29e-99
37	792	44.0	503	4	JQ1321	protein-tyrosine kin	1.04e-98
38	792	44.0	523	1	TVFVMT	protein-tyrosine kin	1.04e-98
39	791	44.0	526	1	TVFV60	protein-tyrosine kin	1.49e-98
40	791	44.0	542	1	TVHUSC	protein-tyrosine kin	1.49e-98
41	792	44.0	543	1	TVHUYS	protein-tyrosine kin	1.04e-98
42	791	44.0	557	1	TVFVS2	protein-tyrosine kin	1.49e-98
43	791	44.0	587	1	TVFVPR	protein-tyrosine kin	1.49e-98
44	792	44.0	590	1	TVFFDS	protein-tyrosine kin	1.04e-98
45	790	43.9	541	4	A43610	protein-tyrosine kin	2.12e-98

ALIGNMENTS

RESULT 1
ENTRY A55625 #type complete
TITLE protein-tyrosine kinase (EC 2.7.1.112),

```
                megakaryocyte-associated - human
ORGANISM        #formal_name Homo sapiens #common_name man
DATE            24-Feb-1995 #sequence_revision 24-Feb-1995 #text_change
                01-Mar-1996
ACCESSIONS      A55625; S43533
REFERENCE       A55625
  #authors      Avraham, S.; Jiang, S.; Ota, S.; Fu, Y.; Deng, B.; Dowler,
                L.L.; White, R.A.; Avraham, H.
  #journal      J. Biol. Chem. (1995) 270:1833-1842
  #title        Structural and functional studies of the intracellular
                tyrosine kinase MATK gene and its translated product.
  #accession    A55625
    ##status        preliminary; not compared with conceptual translation
    ##molecule_type DNA
    ##residues      1-507 ##label AVR
REFERENCE       S43533
  #authors      Sakano, S.; Iwama, A.; Inazawa, J.; Ariyama, T.; Ohno, M.;
                Suda, T.
  #journal      Oncogene (1994) 9:1155-1161
  #title        Molecular cloning of a novel non-receptor tyrosine kinase,
                HYL (hematopoietic consensus tyrosine-lacking kinase).
  #accession    S43533
    ##status        preliminary
    ##molecule_type mRNA
    ##residues      1-507 ##label SAK
    ##cross-references EMBL:X77278
GENETICS
  #gene         GDB:MATK
    ##cross-references GDB:G00-304-667
CLASSIFICATION  #superfamily SH2 homology; protein kinase homology; SH3
                homology
KEYWORDS        phosphotransferase
FEATURE
  55-105            #domain SH3 homology #label SH31\
  122-211           #domain SH2 homology #label SH2\
  233-485           #domain protein kinase homology #label KIN
SUMMARY         #length 507  #molecular-weight 56469  #checksum 6051

  Query Match          100.0%;  Score 1798;  DB 4;  Length 507;
  Best Local Similarity 100.0%;  Pred. No. 3.01e-257;
  Matches   246;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db    233 qhltlgaqigegefgavlqgeylgqkvavknikcdvtaqaflde tavmtkmqhenlvrll 292
          ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Qy    233 QHLTLGAQIGEGEFGAVLQGEYLGQKVAVKNIKCDVTAQAFLDETAVMTKMQHENLVRLL 292

Db    293 gvilhqglyivmehvskgnlvnflrtrgralvntaqllqfslhvaegmeyleskklvhrd 352
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    293 GVILHQGLYIVMEHVSKGNLVNFLRTRGRALVNTAQLLQFSLHVAEGMEYLESKKLVHRD 352

Db    353 laarnilvsedlvakvsdfglakaerkgldssrlpvkwtapealkhgkftsksdvwsfgv 412
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    353 LAARNILVSEDLVAKVSDFGLAKAERKGLDSSRLPVKWTAPEALKHGKFTSKSDVWSFGV 412

Db    413 llwevfsygrapypkmslkevseavekgyrmeppegcpgpvhvlmsscweaeparrppfr 472
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    413 LLWEVFSYGRAPYPKMSLKEVSEAVEKGYRMEPPEGCPGPVHVLMSSCWEAEPARRPPFR 472

Db    473 klaekl 478
          ||||||
Qy    473 KLAEKL 478


RESULT    2
ENTRY           B55625     #type complete
TITLE           protein-tyrosine kinase (EC 2.7.1.112),
```

```
                  megakaryocyte-associated - mouse
ORGANISM          #formal_name Mus musculus #common_name house mouse
DATE              24-Feb-1995 #sequence_revision 24-Feb-1995 #text_change
                  19-Oct-1995
ACCESSIONS        B55625
REFERENCE         A55625
   #authors       Avraham, S.; Jiang, S.; Ota, S.; Fu, Y.; Deng, B.; Dowler,
                  L.L.; White, R.A.; Avraham, H.
   #journal       J. Biol. Chem. (1995) 270:1833-1842
   #title         Structural and functional studies of the intracellular
                  tyrosine kinase MATK gene and its translated product.
   #accession     B55625
      ##status        preliminary; not compared with conceptual translation
      ##molecule_type mRNA
      ##residues      1-465 ##label AVR
CLASSIFICATION    #superfamily SH3 homology; protein kinase homology; SH2
                  homology
KEYWORDS          phosphotransferase
FEATURE
   13-63              #domain SH3 homology #label SH31\
   80-169             #domain SH2 homology #label SH2\
   191-443            #domain protein kinase homology #label KIN
SUMMARY           #length 465  #molecular-weight 51585  #checksum 6919

  Query Match           96.2%;  Score 1730;  DB 4;  Length 465;
  Best Local Similarity  93.9%;  Pred. No. 2.05e-246;
  Matches   231;  Conservative   12;  Mismatches   3;  Indels   0;  Gaps   0;

Db    191 qhltlgaqigegefgavlqgeylgqkvavknikcdvtaqafldetavmtklqhrnlvrll 250
          ||||||||||||||||||||||||||||||||||||||||||||||||||:|| ||||||
Qy    233 QHLTLGAQIGEGEFGAVLQGEYLGQKVAVKNIKCDVTAQAFLDETAVMTKMQHENLVRLL 292

Db    251 gvilhhglyivmehvskgnlvnflrtrgralvstsqllqfalhvaegmeyleskklvhrd 310
          |||||:|||||||||||||||||||||:|:|||||:||||||||||||||||
Qy    293 GVILHQGLYIVMEHVSKGNLVNFLRTRGRALVNTAQLLQFSLHVAEGMEYLESKKLVHRD 352

Db    311 laarnilvsedlvakvsdfglakaerkgldssrlpvkwtapealkngrfssksdvwsfgv 370
          ||||||||||||||||||||||||||||||||||||||||||:|:|:||||||||||
Qy    353 LAARNILVSEDLVAKVSDFGLAKAERKGLDSSRLPVKWTAPEALKHGKFTSKSDVWSFGV 412

Db    371 llwevfsygrapypkmslkevseavekgyrmeppdgcpgsvhtlmgscweaeparrppfr 430
          |||||||||||||||||||||||||||||||:||||:|| ||:||||||||||||||
Qy    413 LLWEVFSYGRAPYPKMSLKEVSEAVEKGYRMEPPEGCPGPVHVLMSSCWEAEPARRPPFR 472

Db    431 kivekl 436
              |: |||
Qy    473 KLAEKL 478


RESULT    3
ENTRY             I48926     #type complete
TITLE             protein-tyrosine kinase (EC 2.7.1.112) Ctk - mouse
ALTERNATE_NAMES   csk-type protein-tyrosine kinase
ORGANISM          #formal_name Mus musculus #common_name house mouse
DATE              15-Mar-1996 #sequence_revision 15-Mar-1996 #text_change
                  15-Mar-1996
ACCESSIONS        I48926
REFERENCE         A53469
   #authors       Klages, S.; Adam, D.; Class, K.; Fargnoli, J.; Bolen, J.B.;
                  Penhallow, R.C.
   #journal       Proc. Natl. Acad. Sci. U.S.A. (1994) 91:2597-2601
   #title         Ctk: a protein-tyrosine kinase related to Csk that defines an
                  enzyme family.
   #cross-references MUID:94195789
   #accession     I48926
      ##status        preliminary
```

```
      ##molecule_type mRNA
      ##residues      1-465 ##label RES
      ##cross-references EMBL:U05210; NID:g450232; CDS_PID:g450233
KEYWORDS         phosphotransferase
SUMMARY          #length 465  #molecular-weight 51495  #checksum 6748

  Query Match           96.2%;  Score 1730;  DB 12;  Length 465;
  Best Local Similarity  93.9%;  Pred. No. 2.05e-246;
  Matches   231;  Conservative   12;  Mismatches   3;  Indels   0;  Gaps   0;

Db    191 qhltlgaqigegefgavlqgeylgqkvavknikcdvtaqaflde-tavmtklqhrnlvrll 250
          ||||||||||||||||||||||||||||||||||||||||||||||:|| ||||||
Qy    233 QHLTLGAQIGEGEFGAVLQGEYLGQKVAVKNIKCDVTAQAFLDETAVMTKMQHENLVRLL 292

Db    251 gvilhhglyivmehvskgnlvnflrtrgralvstsqllqfalhvaegmeyleskklvhrd 310
          |||||:|||||||||||||||||||||:|:|||||:||||||||||||||||
Qy    293 GVILHQGLYIVMEHVSKGNLVNFLRTRGRALVNTAQLLQFSLHVAEGMEYLESKKLVHRD 352

Db    311 laarnilvsedlvakvsdfglakaerkgldssrlpvkwtapealkngrfssksdvwsfgv 370
          ||||||||||||||||||||||||||||||||||||||||||:|:|:||||||||||
Qy    353 LAARNILVSEDLVAKVSDFGLAKAERKGLDSSRLPVKWTAPEALKHGKFTSKSDVWSFGV 412

Db    371 llwevfsygrapypkmslkevseavekgyrmeppdgcpgsvhtlmgscweaeparrppfr 430
          ||||||||||||||||||||||||||||||||:||||:|| ||:|||||||||||||
Qy    413 LLWEVFSYGRAPYPKMSLKEVSEAVEKGYRMEPPEGCPGPVHVLMSSCWEAEPARRPPFR 472

Db    431 kivekl 436
          |: |||
Qy    473 KLAEKL 478


RESULT    4
ENTRY            A49865     #type complete
TITLE            protein-tyrosine kinase (EC 2.7.1.112) matk - human
ALTERNATE_NAMES  megakaryocyte-associated tryosine kinase
ORGANISM         #formal_name Homo sapiens #common_name man
DATE             30-Jun-1995 #sequence_revision 30-Jun-1995 #text_change
                   19-Oct-1995
ACCESSIONS       A49865
REFERENCE        A49865
   #authors      Bennett, B.D.; Cowley, S.; Jiang, S.; London, R.; Deng, B.;
                   Grabarek, J.; Groopman, J.E.; Goeddel, D.V.; Avraham, H.
   #journal      J. Biol. Chem. (1994) 269:1068-1074
   #title        Identification and characterization of a novel tyrosine
                   kinase from megakaryocytes.
   #accession    A49865
      ##status        preliminary
      ##molecule_type mRNA
      ##residues      1-527 ##label BEN
      ##cross-references GB:L18974
CLASSIFICATION   #superfamily SH2 homology; protein kinase homology; SH3
                   homology
KEYWORDS         phosphotransferase
FEATURE
   55-105             #domain SH3 homology #label SH31\
   122-211            #domain SH2 homology #label SH2\
   233-484            #domain protein kinase homology #label KIN
SUMMARY          #length 527  #molecular-weight 58473  #checksum 1630

  Query Match           93.6%;  Score 1683;  DB 11;  Length 527;
  Best Local Similarity  99.1%;  Pred. No. 6.22e-239;
  Matches   232;  Conservative    1;  Mismatches   0;  Indels   1;  Gaps   1;

Db    233 qhltlgaqigegefgavlqgeylgqkvavknikcdvtaqaflde-tavmtkmqhenlvrll 292
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    233 QHLTLGAQIGEGEFGAVLQGEYLGQKVAVKNIKCDVTAQAFLDETAVMTKMQHENLVRLL 292
```

```
Db    293 gvilhqglyivmehvskgnlvnflrtrgralvntaqllqfslhvaegmeyleskklvhrd 352
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    293 GVILHQGLYIVMEHVSKGNLVNFLRTRGRALVNTAQLLQFSLHVAEGMEYLESKKLVHRD 352

Db    353 laarnilvsedlvakvsdfglakaerkgldssrlpvkwtapealkhg-ftsksdvwsfgv 411
          |||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Qy    353 LAARNILVSEDLVAKVSDFGLAKAERKGLDSSRLPVKWTAPEALKHGKFTSKSDVWSFGV 412

Db    412 llwevfsygrapypkmslkevseavekgyrmeppegcpgpvhvlmsscweaepp 465
          |||||||||||||||||||||||||||||||||||||||||||||||||||||:
Qy    413 LLWEVFSYGRAPYPKMSLKEVSEAVEKGYRMEPPEGCPGPVHVLMSSCWEAEPA 466


RESULT    5
ENTRY           A41973     #type fragment
TITLE           protein-tyrosine kinase (EC 2.7.1.112) CSK - chicken
                  (fragment)
ORGANISM        #formal_name Gallus gallus #common_name chicken
DATE            31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change
                  12-Apr-1995
ACCESSIONS      A41973
REFERENCE       A41973
   #authors     Sabe, H.; Knudsen, B.; Okada, M.; Nada, S.; Nakagawa, H.;
                  Hanafusa, H.
   #journal     Proc. Natl. Acad. Sci. U.S.A. (1992) 89:2190-2194
   #title       Molecular cloning and expression of chicken C-terminal Src
                  kinase: lack of stable association with c-Src protein.
   #cross-references MUID:92196083
   #accession   A41973
      ##status        preliminary
      ##molecule_type DNA
      ##residues      1-450 ##label SAB
      ##cross-references NCBIN:88058; NCBIP:88059
      ##note          sequence extracted from NCBI backbone
CLASSIFICATION  #superfamily protein-tyrosine kinase src; protein kinase
                  homology; SH2 homology; SH3 homology
KEYWORDS        ATP; phosphotransferase; tyrosine-specific protein kinase
FEATURE
   16-65            #domain SH3 homology #label SH3\
   82-171           #domain SH2 homology #label SH2\
   193-447          #domain protein kinase homology #label KIN\
   201-209          #region protein kinase ATP-binding motif
SUMMARY         #length 450  #checksum 7

  Query Match           64.5%;  Score 1160;  DB 4;  Length 450;
  Best Local Similarity 59.3%;  Pred. No. 3.91e-156;
  Matches  146;  Conservative  50;  Mismatches 48;  Indels  2;  Gaps  1;

Db    195 lkllqiigkgefgdvalgdyrgnkvavkcikndataqaflaeasvmtqlrhsnlvqllgv 254
          | |   || |||| |: |:| | ||||| || | |||||| |::||| ::| |||:||||
Qy    235 LTLGAQIGEGEFGAVLQGEYLGQKVAVKNIKCDVTAQAFLDETAVMTKMQHENLVRLLGV 294

Db    255 iveeksglyivteymakgslvdylrsrgrsvlggdcllkfsldvceameyleannfvhrd 314
          |: :  ||||| | ::||:||::||:|||::    || ||| | |:|||||::::|||| 
Qy    295 ILHQ--GLYIVMEHVSKGNLVNFLRTRGRALVNTAQLLQFSLHVAEGMEYLESKKLVHRD 352

Db    315 laarnvlvsedniakvsdfgltkeasstqdtgklpvkwtapealrekkfstksdvwsfgi 374
          |||||:|||||  :|||||||:|      |:::|||||||||||:  ||::|||||||:
Qy    353 LAARNILVSEDLVAKVSDFGLAKAERKGLDSSRLPVKWTAPEALKHGKFTSKSDVWSFGV 412

Db    375 llweiysfgrvpypriplkdvvprvekgykmdppdgcpaivyevmkkcwtldpghrpsfh 434
          ||||::|:|| |||:::||:|   |||||:|:||:|||: |  :|  ||  :|::||:|:
Qy    413 LLWEVFSYGRAPYPKMSLKEVSEAVEKGYRMEPPEGCPGPVHVLMSSCWEAEPARRPPFR 472

Db    435 qlreql 440
```

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#####
#####
#####
#####
#####       User: stic9!shears
#####
#####      Title: US-08-426-509-2-01.rag
#####
#####              stic9
#####
#####    Printed: Tue 09:25 Feb 04, 1997
#####
##### Job number: MT691-154
#####
#####
#####
#####
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      ___     ___     _______     _____     ______     _____     _       _
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     | |\ \ / /| |   | |   | |   | |       | |  | |   | |       | |     | |
     | | \_\/ | |   | |___| |   | |___    | |__| |   | |       | |___  | |
     | |       | |   |  _____|   |___  |   |    __|   | |       |  ___  |
     | |       | |   | |               | |   | |\ \    | |       | |   | |
     | |       | |   | |           ___| |   | | \ \   | |___    | |   | |
     |_|       |_|   |_|          |_____|   |_|  \_\  |_____|   |_|   |_|   (TM)

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